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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/142,108C

DATE: 05/16/2002

TIME: 16:07:34

Input Set : A:\11658.asc

Output Set: N:\CRF3\05162002\I142108C.raw

4 <110> APPLICANT: Brugliera, Filippa
 5 Holton, Timothy A.
 6 Michael, Michael Z.
 8 <120> TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
 9 AND USES THEREFOR
 11 <130> FILE REFERENCE: 11658
 13 <140> CURRENT APPLICATION NUMBER: 09/142,108C
 14 <141> CURRENT FILING DATE: 1998-09-01
 16 <150> PRIOR APPLICATION NUMBER: PN8386
 17 <151> PRIOR FILING DATE: 1996-03-01
 19 <160> NUMBER OF SEQ ID NOS: 45
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1789
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Petunia x hybrida
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (50)..(1588)
 32 <400> SEQUENCE: 1
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 34 Met Glu Ile
 35 1
 37 tta agc cta att ctg tac acc gtc att ttc tca ttt ctt cta caa ttc 106
 38 Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe
 39 5 10 15
 41 att ctt aga tca ttt ttc cgt aaa cgt tac cct tta cca tta cca cca 154
 42 Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro
 43 20 25 30 35
 45 ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202
 46 Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
 47 40 45 50
 49 aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250
 50 Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu
 51 55 60 65
 53 atg tat ctt aag atg ggg ttc gta gac gtg gtg gtt gca gcc tcg gca 298
 54 Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
 55 70 75 80
 57 tcg gtt gca gct cag ttc ttg aaa act cat gat gct aat ttc tcg agc 346
 58 Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser Ser
 59 85 90 95
 61 cgt cca cca aat tct ggt gca gaa cat atg gct tat aat tat cag gat 394
 62 Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln Asp

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Input Set : A:\11658.asc

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66	Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile							
67			120		125		130	
69	tgc tca gtt cac ctt ttc tct acc aag gct tta gat gac ttc cgc cat	490						
70	Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His							
71			135		140		145	
73	gtc cgc cag gat gaa gtg aaa aca ctg acg cgc gca cta gca agt gca	538						
74	Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser Ala							
75			150		155		160	
77	ggc caa aag cca gtc aaa tta ggt cag tta ttg aac gtg tgc acg acg	586						
78	Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr							
79			165		170		175	
81	aac gca ctc gcg cga gta atg cta ggt aag cga gta ttt gcc gac gga	634						
82	Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp Gly							
83	180		185		190		195	
85	agt ggc gat gtt gat cca caa gcg gcg gag ttc aag tca atg gtg gtg	682						
86	Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val							
87			200		205		210	
89	gaa atg atg gta gtc gcc ggt gtt ttt aac att ggt gat ttt att ccg	730						
90	Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp Phe Ile Pro							
91			215		220		225	
93	caa ctt aat tgg tta gat att caa ggt gta gcc gct aaa atg aag aag	778						
94	Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys Met Lys Lys							
95			230		235		240	
97	ctc cac gcg cgt ttc gac gcg ttc ttg act gat ata ctt gaa gag cat	826						
98	Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu Glu Glu His							
99			245		250		255	
101	aag ggt aaa att ttt gga gaa atg aaa gat ttg ttg agt act ttg atc	874						
102	Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser Thr Leu Ile							
103	260		265		270		275	
105	tct ctt aaa aat gat gat gcg gat aat gat gga ggg aaa ctc act gat	922						
106	Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys Leu Thr Asp							
107			280		285		290	
109	aca gaa att aaa gca tta ctt ttg aac ttg ttt gta gct gga aca gac	970						
110	Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala Gly Thr Asp							
111			295		300		305	
113	aca tct tct agt aca gtt gaa tgg gcc att gct gag ctt att cgt aat	1018						
114	Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn							
115			310		315		320	
117	cca aaa ata cta gcc caa gcc cag caa gag atc gac aaa gtc gtt gga	1066						
118	Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys Val Val Gly							
119			325		330		335	
121	agg gac cgg cta gtt ggc gaa ttg gac cta gcc caa ttg aca tac ttg	1114						
123	Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu Thr Tyr Leu							
124	340		345		350		355	
126	gaa gct ata gtc aag gaa acc ttt cgg ctt cat cca tca acc cct ctt	1162						
127	Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu							
128			360		365		370	

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130 tca ctt cct aga att gca tct gag agt tgt gag atc aat ggc tat ttc 1210
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132          375          380          385
134 att cca aaa ggc tca acg ctt ctc ctt aat gtt tgg gcc att gct cgt 1258
135 Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala Ile Ala Arg
136          390          395          400
138 gat cca aat gca tgg gct gat cca ttg gag ttt agg cct gaa agg ttt 1306
139 Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe
140          405          410          415
142 ttg cca gga ggt gag aag ccc aaa gtt gat gtc cgt ggg aat gac ttt 1354
143 Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly Asn Asp Phe
144 420          425          430          435
146 gaa gtc ata cca ttt gga gct gga cgt agg att tgt gct gga atg aat 1402
147 Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Asn
148          440          445          450
150 ttg ggt ata cgt atg gtc cag ttg atg att gca act tta ata cat gca 1450
151 Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu Ile His Ala
152          455          460          465
154 ttt aac tgg gat ttg gtc agt gga caa ttg ccg gag atg ttg aat atg 1498
155 Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met Leu Asn Met
156          470          475          480
158 gaa gaa gca tat ggg ctg acc tta caa cgg gct gat cca ttg gtt gtg 1546
159 Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro Leu Val Val
160          485          490          495
162 cac cca agg cct cgc tta gaa gcc caa gcg tac att ggg tga 1588
163 His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
164 500          505          510
166 gcagcaacag cccatggaga taacatgagt gttaaagtga tgagtctcca tatcttgttt 1648
168 agtttggtta tgctttggat ttagtagttt ttatattgat agatcaatgt ttgcattgtc 1708
170 agtaagaata tccgttgctt gtttcattaa ctccaggtgg acaataaaaag aagtaatttg 1768
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178 <213> ORGANISM: Petunia x hybrida
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185 20 25 30
186 Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His
187 35 40 45
188 Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr
189 50 55 60
190 Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala
191 65 70 75 80
192 Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn
193 85 90 95
194 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn

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195          100          105          110
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198 Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp
199          130          135          140
200 Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu
201 145          150          155          160
202 Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val
203          165          170          175
204 Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
205          180          185          190
206 Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser
207          195          200          205
208 Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
209          210          215          220
210 Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys
211 225          230          235          240
212 Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu
213          245          250          255
214 Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser
215          260          265          270
216 Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys
217          275          280          285
218 Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala
219          290          295          300
220 Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu
221 305          310          315          320
222 Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys
223          325          330          335
224 Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu
225          340          345          350
226 Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser
227          355          360          365
228 Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn
229          370          375          380
230 Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala
231 385          390          395          400
232 Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro
233          405          410          415
234 Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly
235          420          425          430
236 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala
237          435          440          445
238 Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu
239          450          455          460
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240 Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met
241 465          470          475          480
242 Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro
243          485          490          495

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Input Set : A:\11658.asc

Output Set: N:\CRF3\05162002\I142108C.raw

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251 <211> LENGTH: 1737
252 <212> TYPE: DNA
253 <213> ORGANISM: Dianthus caryophyllus
256 <220> FEATURE:
257 <221> NAME/KEY: CDS
258 <222> LOCATION: (172)..(1674)
260 <400> SEQUENCE: 3
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265 aaaaaaaatt ataatgtcac ccttagaggt aactttctac accatagtcc t atg cac 177
266                                     Met His
267                                     1
269 aat ctc tac tac ctc atc acc acc gtc ttc cgc ggc cac caa aaa ccg 225
270 Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro
271          5                      10                      15
273 ctt cct cca ggg cca cga cca tgg ccc atc gtg gga aac ctc cca cat 273
274 Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His
275          20                      25                      30
277 atg ggc cag gca ccg cac cag ggc tta gca gcc ctg gcg caa aag tat 321
278 Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr
279          35                      40                      45                      50
281 ggc cct cta ttg tat atg aga ctg ggg tac gtg gac gtt gtt gtg gcc 369
282 Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val Val Ala
283          55                      60                      65
285 gcc tca gcg tct gta gcg acc cag ttt ctt aag aca cat gac cta aat 417
286 Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp Leu Asn
287          70                      75                      80
289 ttt tcg agt agg cca ccg aat tcg ggg gct aaa cac att gct tat aac 465
290 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala Tyr Asn
291          85                      90                      95
293 tat caa gac ctt gtt ttt gca cct tat gga cct aaa tgg cgc atg ctt 513
294 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu
295          100                     105                     110
297 agg aaa att tgt tcc tta cac atg ttt tct tct aag gct ttg gac gat 561
298 Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp
299          115                     120                     125                     130
301 ttt aga ctt gtc cgt cag gaa gaa gta tct ata ctg gta aat gcg ata 609
302 Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn Ala Ile
303          135                     140                     145
305 gca aaa gca gga aca aag cca gta caa cta gga caa cta ctc aac gtg 657
307 Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu Asn Val
308          150                     155                     160
310 tgc acc aca aat gcc tta tcg agg gtg atg cta ggg aag cga gtt ctc 705
311 Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg Val Leu
312          165                     170                     175
314 ggt gat ggc aca ggg aaa agc gac cca aaa gcc gag gaa ttt aag gac 753

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/142,108C

DATE: 05/16/2002
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Input Set : A:\11658.asc

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:33; N Pos. 11,14,20
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Seq#:36; N Pos. 3,7,8,9,12,15,18
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Seq#:44; Xaa Pos. 8,10,15
Seq#:45; Xaa Pos. 8,10,15,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33
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VERIFICATION SUMMARY

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Output Set: N:\CRF3\05162002\I142108C.raw

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L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:2887 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:2909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:2921 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2926 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2931 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2936 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2941 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2946 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2951 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:3000 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3005 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3010 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40

VERIFICATION SUMMARY

DATE: 05/16/2002

PATENT APPLICATION: US/09/142,108C

TIME: 16:07:35

Input Set : A:\11658.asc

Output Set: N:\CRF3\05162002\I142108C.raw

L:3015 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3020 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3025 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3030 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:3248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:3282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:3285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:16
L:3288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:32
L:3291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:48
L:3294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:64
L:3297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:80
L:3300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:96
L:3303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:112
L:3306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:128
L:3309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:144
L:3312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:160
L:3315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:176
L:3318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:192
L:3321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:208
L:3324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:224
L:3327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:240
L:3330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:256
L:3333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:272
L:3336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:288
L:3339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:304
L:3342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:320
L:3345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:336
L:3348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:352
L:3351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:368
L:3354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:384
L:3357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:400
L:3360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:416
L:3363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:432
L:3366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:448
L:3370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:464
L:3373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:480
L:3376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:496
L:3379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:512